

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: November 7, 2004, 05:29:17 ; Search time 6565 seconds
(without alignments)
11589.666 Million cell updates/sec

Title: US-09-679-687b-1

Perfect score: 1 gacagagacactccctaccc.....aaaaaaaaaaaaaaaaaaaaa 2088

Sequence: IDENTITY_NTC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

EST.*
1: gb_esc1.*
2: gb_esc2.*
3: gb_ntc.*
4: gb_esc3.*
5: gb_esc4.*
6: gb_esc5.*
7: gb_esc6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2088	100.0	2088	3	AY106212 Zea mays
2	850.6	40.7	902	6	CD440318 ELO1N0553
3	790.4	37.9	895	6	CD441187 ELO1N0553
4	630.6	30.2	1071	7	CK162907 FGAS01551
5	546	26.1	669	6	CD434724 ELO1N0327
6	539.6	25.8	847	6	CB647418 OSJNB10F
7	531.8	25.5	854	6	CA195914 SCZAD108
8	523.8	25.1	705	5	BU925783 MCSA174E1
9	518.6	24.8	811	6	CB659941 OSJNB01E
10	516.4	24.7	843	6	CB661694 OSJNB01E
11	508	24.3	688	6	CD236385 S61_33_G1
12	495	23.7	589	6	CA399941 ELO1N0327
13	493.8	23.6	769	6	CB678068 OSJNB01E
14	490.8	23.5	742	6	CB618707 OSJNB01E
15	488.8	23.4	719	5	BU925792 MCSA179A0
16	484.8	23.2	496	5	BO538253 MEST599-A
17	480.2	23.0	587	2	BE361547 DGL_81_H0
18	476.8	22.8	651	6	CP325968 WMT--54-
19	463	22.9	998	7	CK162767 RGA901536
20	457.2	22.9	694	6	CD881813 F1.104P23
21	445	21.3	538	6	CA220149 SCRUF1402
22	437.8	21.3	657	7	CN150206 WOUNDI_67
23	437.8	21.0	656	6	CD879901 ACO4_106L
24	433.8	20.8	539	6	CA163799 SCRUM2308

25	433.2	20.7	704	6	CD884481 F1.116N07
26	432.4	20.5	594	2	BP478755 WHE2013_C
27	429	20.5	532	7	CF630902 ZMR648_0
28	429	20.5	647	1	AV925143 AV925143
29	425.8	20.4	533	7	CK359825 ZMR6485
30	422.6	20.2	592	6	BQ743802 WHE4108_C
31	422.4	20.2	526	6	CD970384 QAD1609_C
32	422.4	20.2	526	6	CD970384 QAD1609_C
33	420.6	20.1	617	4	BJ477966 BJ477966
34	416.4	19.9	482	1	BG837732 Zml0_05d0
35	414.2	19.8	700	4	AL508285 AL508285
36	411.8	19.7	518	2	BE360821 DGL_67_H0
37	411.6	19.7	828	4	BI953334 HYSEM001
38	411.4	19.7	795	7	CO522314 3510_1_14
39	411.2	19.7	828	7	CC692415 OGUC61TH
40	409.8	19.6	768	7	CO527407 3510_1_18
41	409.4	19.6	731	7	CK124551 BE3182410
42	403.8	19.3	587	6	CA222528 SCBFL405
43	402.4	19.3	516	7	CK371610 ZMRW005
44	396.2	19.0	757	8	B2638091 OGCA677C
45	393	18.8	582	6	CD057532 HO15G165

ALIGNMENTS

RESULT 1
LOCUS AY106212 2088 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO103031 mRNA sequence.
ACCESSION AY106212
VERSION AY106212.1 GI:21209290
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

1. Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., White, M.S.,
Arthur, L.W., Hanley, M., Morgan, M., and Tingey, S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2. (bases 1 to 2088)
Coe, E.H.

COMMENT

Direct Submission
Submitted (25-Apr-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schubert, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES

1. 2088
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dupont Consensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Query Match 100.0%; Score 2088; DB 3; Length 2088;